Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application. These amendments are based on the wording of the claims *prior* to the Amendment filed on June 25, 2003, as this Amendment was not entered (see Advisory Action mailed July 16, 2003).

Listing of Claims:

1-20. (canceled)

21. (currently amended) An ~~array,~~ array comprising a plurality of sets of nucleic acid probes, each set comprising a plurality of probe pools bound to a different region of a support, each pool comprising (i) a first probe that is ~~common to the probe pools within the set and~~ complementary to a known marker located in a target nucleic ~~acid;~~ acid, and (ii) a second probe that differs in sequence from the first probe; and wherein ~~the~~ first probes ~~differ in sequence between the different sets~~ within the same set have the same sequence but first probes in different sets have different sequences.

22. (previously presented) The array of claim 21, wherein the first probes in different sets are complementary to different markers on the target nucleic acid.

23. (currently amended) The array of claim 21, wherein ~~for any particular set of probes the~~ second probes within the same set are the same length and collectively represent all possible sequences having that length.

24. (currently amended) An array comprising a set of nucleic acid probes, the set comprising a plurality of different nucleic acid probe mixtures bound to different regions of a support, each mixture comprising an interrogation probe and a partner probe, wherein

the interrogation probes are complementary to a first segment of a reference nucleic acid that contains an interrogation ~~position and~~ position;

interrogation probes at different regions are identical to one another except at the interrogation position, with ~~different~~ interrogation probes at different regions having a different nucleotide base at the interrogation position; and

the partner probe is complementary to a second segment of the reference nucleic acid that does not overlap the first segment~~; and~~

~~different probe mixtures have different interrogation probes~~.

25. (previously presented) The array of claim 24, wherein different probe mixtures contain the same partner probe.

26. (currently amended) The array of claim 24, wherein different probe mixtures contain different partner probes that ~~bind~~ are complementary to different second segments.

27. (currently amended) The array of claim 24, wherein the interrogation probes and partner probes are complementary to ~~the~~ first and second segments that are separated from one another on the reference ~~sequence~~ nucleic acid.

28. (currently amended) The array of claim 24, wherein the interrogation probes and partner probes are complementary to ~~the~~ first and second segments that are immediately adjacent one another on the reference ~~sequence~~ nucleic acid.

29. (canceled)

30. (currently amended) A method for analyzing a target nucleic acid sequence, comprising

(a) providing an array comprising a set of nucleic acid probes, the set comprising a plurality of different nucleic acid probe mixtures bound to different regions of a support, each mixture comprising an interrogation probe and a partner probe, wherein

the interrogation probes are complementary to a first segment of a reference nucleic acid that contains an interrogation position;

interrogation probes at different regions are ~~and~~ identical to one another except at the interrogation position, with ~~different~~ interrogation probes at different regions having a different ~~one of the four~~ nucleotide ~~bases~~ base at the interrogation position; and

the partner probe is complementary to a second segment of the reference nucleic acid that does not overlap the first segment; ~~and~~

~~different probe mixtures have different interrogation probes;~~

(b) applying a sample comprising a target nucleic acid to the array; and

(c) determining the identity of the nucleotide base at the interrogation position of the target nucleic acid from the relative binding of the target nucleic acid to the different probe mixtures.

31. (new) The array of claim 24, wherein the set of nucleic acid probes comprises four different nucleic acid probe mixtures, with interrogation probes in different mixtures having a different one of the four nucleotide bases at the interrogation position.